IN THE SPECIFICATION:

Please amend paragraph [0002] of the specification as filed (paragraph [0002] ***as published***) as follows:

[0002] The present invention relates to a method for the in vitro differentiation between systemic inflammatory non-infectious conditions and systemic inflammatory infectious conditions ~~according to claim 1~~.

Please amend paragraphs [0026]-[0028] of the specification as filed (paragraphs [0025]-[027] ***as published***) as follows:

[0026] This task is solved by a process as set forth in the claims ~~with the characterizing features of claim 1~~.

[0027] ~~The invention is further concerned with the task of providing a possibility of use of markers in a process according to claim 1-25~~.

[0028] ~~This task is solved by the use according to claims 26-32~~.

Please amend paragraph [0039] of the specification as filed (paragraph [0042] ***as published***) as follows:

[0039] These sequences with a sequence ID: 1 through sequence ID: 91 are included within the scope of the present invention and are disclosed in detail in the attached 42-page, 91-sequence-covering sequence protocol which therewith becomes part of the invention. This sequence protocol includes, besides this, classification or correlation of the individual sequences with the sequence ID: 1 through sequence ID: 91 to their GeneBank Accession No. ~~(Internet access via www.ncbi.nim.nih.gov/).~~

Please amend paragraph [0063] of the specification as filed (paragraph [0067] ***as published***) as follows:

[0063]A further application of the inventive process is comprised in the measurement of the differential gene expression for therapy accompanying determination of the probability whether patients would respond to the planned therapy, and/or for the determination of the response to the specialized therapy and/or on the determination of the therapy termination in the sense of a "drug monitoring" in patients with SIRS and sepsis. For this, the RNA (sample RNA) is isolated from blood samples collected over time from the patients. The different RNA samples are marked together with the control sample and are hybridized with selected genes ~~according to claim 10~~, which are immobilized on a microarray. From the respective expression relationships it can be evaluated or determined which probability there is that patients would respond to a planned therapy and/or whether the initiated therapy would be effective and/or the length to which patients still need to be subject to therapy and/or whether the maximal therapeutic effect has already been achieved with the employed dosing and duration.

Please amend paragraph [0068] of the specification as filed (paragraph [0071] ***as published***) as follows:

[0068] Whole blood samples of five male and one female patient were obtained (patient samples). Each of these patients developed sepsis in the framework of their intensive medical intervention following a by-pass operation. The patient samples were drawn immediately (within 12 hours) after initial diagnosis of sepsis corresponding to the classification according to [1] was obtained. Selective characteristics of the patients with sepsis are indicated in Table 1. Therein, indications regarding age, sex, cause of sepsis (see diagnosis as well as clinical acuteness), measured according to--in clinical literature well documented--APACHE-II- and SPFA-Scores (respectively in Dots) was made. Likewise the plasma protein level of procalcitonin (PCT), a more recent sepsis marker, the Center for Disease (CDC)-criteria ~~(see http://www.cdc.gov)~~ and the individual survival status are indicated.

Please amend paragraph [0081] of the specification as filed (paragraph [0084] ***as published***) as follows:

[0081] The GenBank Acccession Numbers indicated in Tables 2 and 3 ~~(Internet-access via http://www.ncbi.nlm.nih.gov/)~~ of the individual sequences associated with the attached 42-page sequence protocol of the present application, which is therewith part of the invention, itemized or in detail with respectively one sequence (Sequence ID: 1 up through Sequence ID: 91). This sequence protocol is part of the present invention.